

SEQUENCE LISTING

#1

(1) GENERAL INFORMATION:

(i) APPLICANT: WALLACH, DAVID
NOPHAR, YARON
KEMPER, OLIVER
ENGELMANN, HARTMUT
BRAKEBUSCH, CORD
ADERKA, DAN

(ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Browdy and Neimark
(B) STREET: 419 Seventh Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/625668
(B) FILING DATE: 13-DEC-1990
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 25,618
(C) REFERENCE/DOCKET NUMBER: WALLACH4

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 256..1620

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 319..1620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGCCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60
GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCCC 120
GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180
CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240
CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro
-21 -20 -15 -10
CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339
Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile
-5 1 5
GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387
Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys
10 15 20
CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435
Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
25 30 35
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly
40 45 50 55

39

CAG	GAT	ACG	GAC	TGC	AGG	GAG	TGT	GAG	AGC	GGC	TCC	TTC	ACC	GCT	TCA	531
Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	
				60					65					70		
GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	AAA	TGC	CGA	AAG	GAA	579
Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	
			75					80					85			
ATG	GGT	CAG	GTG	GAG	ATC	TCT	TCT	TGC	ACA	GTG	GAC	CGG	GAC	ACC	GTG	627
Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	
		90					95					100				
TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	TGG	AGT	GAA	AAC	CTT	675
Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	
	105					110					115					
TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	ACC	GTG	CAC	CTC	723
Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	
120					125					130					135	
TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	CAT	GCA	GGT	TTC	771
Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	
				140				145					150			
TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	819
Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	
			155					160					165			
CTG	GAG	TGC	ACG	AAG	TTG	TGC	CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	867
Leu	Glu	Cys	Thr	Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	
		170				175						180				
ACT	GAG	GAC	TCA	GGC	ACC	ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	915
Thr	Glu	Asp	Ser	Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	
	185					190					195					
GGT	CTT	TGC	CTT	TTA	TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	963
Gly	Leu	Cys	Leu	Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	
200					205					210					215	
CAA	CGG	TGG	AAG	TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	1011
Gln	Arg	Trp	Lys	Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	
				220				225					230			
CCT	GAA	AAA	GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	1059
Pro	Glu	Lys	Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	
			235					240					245			
CCA	AAC	CCA	AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	1107
Pro	Asn	Pro	Ser	Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	
		250					255					260				

TTC	AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC	1155
Phe	Ser	Pro	Val	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	
265						270					275					
CCC	GGT	GAC	TGT	CCC	AAC	TTT	GCG	GCT	CCC	CGC	AGA	GAG	GTG	GCA	CCA	1203
Pro	Gly	Asp	Cys	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	
280					285					290					295	
CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC	TCC	GAC	1251
Pro	Tyr	Gln	Gly	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	
				300					305					310		
CCC	ATC	CCC	AAC	CCC	CTT	CAG	AAG	TGG	GAG	GAC	AGC	GCC	CAC	AAG	CCA	1299
Pro	Ile	Pro	Asn	Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	
			315					320					325			
CAG	AGC	CTA	GAC	ACT	GAT	GAC	CCC	GCG	ACG	CTG	TAC	GCC	GTG	GTG	GAG	1347
Gln	Ser	Leu	Asp	Thr	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	Ala	Val	Val	Glu	
		330					335					340				
AAC	GTG	CCC	CCG	TTG	CGC	TGG	AAG	GAA	TTC	GTG	CGG	CGC	CTA	GGG	CTG	1395
Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	
345						350					355					
AGC	GAC	CAC	GAG	ATC	GAT	CGG	CTG	GAG	CTG	CAG	AAC	GGG	CGC	TGC	CTG	1443
Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	
360					365					370					375	
CGC	GAG	GCG	CAA	TAC	AGC	ATG	CTG	GCG	ACC	TGG	AGG	CGG	CGC	ACG	CCG	1491
Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Thr	Pro	
				380					385					390		
CGG	CGC	GAG	GCC	ACG	CTG	GAG	CTG	CTG	GGA	CGC	GTG	CTC	CGC	GAC	ATG	1539
Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	
			395					400					405			
GAC	CTG	CTG	GGC	TGC	CTG	GAG	GAC	ATC	GAG	GAG	GCG	CTT	TGC	GGC	CCC	1587
Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	Ile	Glu	Glu	Ala	Leu	Cys	Gly	Pro	
		410					415					420				
GCC	GCC	CTC	CCG	CCC	GCG	CCC	AGT	CTT	CTC	AGA	TGAGGCTGCG	CCCTGCGGGC				1640
Ala	Ala	Leu	Pro	Pro	Ala	Pro	Ser	Leu	Leu	Arg						
425						430										
AGCTCTAAGG	ACCGTCCTGC	GAGATCGCCT	TCCAACCCCA	CTTTTTTTCTG	GAAAGGAGGG											1700
GTCCTGCAGG	GGCAAGCAGG	AGCTAGCAGC	CGCCTACTTG	GTGCTAACCC	CTCGATGTAC											1760
ATAGCTTTTC	TCAGCTGCCT	GCGCGCCGCC	GACAGTCAGC	GCTGTGCGCG	CGGAGAGAGG											1820

TCGCCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTTGCGAG GATGAGGGAC GCTATGCCTC 1880
 ATGCCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCCCTGGT TCGTCCCTGA 1940
 GCCTTTTTTCA CAGTGCATAA GCAGTTTTTTT TTGTTTTTGT TTTGTTTTGT TTTGTTTTTA 2000
 AATCAATCAT GTTACACTAA TAGAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA 2060
 CATAGCAAGC TGAAGTGTCC TAAGGCAGGG GCGAGCACGG AACAATGGGG CCTTCAGCTG' 2120
 GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAA 2175

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 -21 -20 -15 -10
 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 -5 1 5 10
 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 15 20 25
 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 30 35 40
 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 45 50 55
 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 60 65 70 75
 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
 80 85 90
 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
 95 100 105
 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
 110 115 120

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
 125 130 135
 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
 140 145 150 155
 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
 160 165 170
 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
 175 180 185
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
 190 195 200
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
 205 210 215
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
 220 225 230 235
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
 240 245 250
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
 255 260 265
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
 270 275 280
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
 285 290 295
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
 300 305 310 315
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
 320 325 330
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
 335 340 345
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
 350 355 360
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
 365 370 375
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
 380 385 390 395

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
400 405 410

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
415 420 425

Pro Ala Pro Ser Leu Leu Arg
430

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNGTYCCNT TYATRTARGET DGGNGT

26

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGNGTYCCNT TYATRTA

17

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTYATRTARG TDGGNGT

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGCCGATGG GCCTCTCCAC CGTGCCT

27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATAGTATTT CTAATCTGGG GTAGGCA

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Ser Val Cys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTCATGGA TAGTGTGTGT CCC

23

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACCTATCA CACACAGGGG TTC

23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
1 5 10 15
Arg Leu Arg Glu Tyr Tyr
 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Cys Ala Pro Leu Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Arg Pro Gly Phe Gly Val Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Cys Gly Pro Ser Tyr Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Gly Trp Tyr Cys Ala Leu Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Arg Pro Gly Phe Gly Val Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly
1 5 10 15

Thr Phe Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp
1 5 10 15
Val Val Cys Lys
20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
1 5 10 15
Leu Trp

TBP I:
CNBr-1 (=N-terminus)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
NH ₂	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	-	
	(Seq. ID No.: 2, amino acids 41-53)														

NH₂ Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val
 (Seq. ID No.: 2, amino acids 110-124)

C-terminus

Ile Glu Asn COOH

TBP II:

N-terminus

[illegible]